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Best Local Sim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                        ttttaagcactgaatatcgaacaagcactcaaattgaagtatcagtcatgttttgtgtat 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1105 ttttcgctgataaaaattatttaacatttatattttacttgattacatatgcacatgta 1164
                                                                                                                                                                                                                                866 cttcctttccgattcttcatccggtctacggctatgcaattcctccccaaatatagatct 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 TTTTAAGCACTGAATATCGAACAACAAGCACTCAAATTGAAGTATCAGTCATGTTTTTTGTGTAT 164
                                                                                                                                                                                                                                                                                                            402 CTTCCTTTCCGATTCTTCATCCGGTCTAC-GCTATGCAATTCCTCCCCAAATATAGATCT 344
                                                                                                                                                                                                                                                                                                                                     926 tatttctgctcatttcccctacttattaaaatcacaccaaacacttactattttcttatc 985
                                                                                                                                                                                                                                                                                                                                                               343 TATTTCTGCTCATTTCCCCTACTTATTAAAATCACACCAAACACTTACTATTTTCTTATC
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NCI-OGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project ((
                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                 Length 462;
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9;
                                                                                                                                                                               Score 429.6; DB 9
Pred. No. 1.7e-37;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
/lab_host-"DH10B'
                                                                                                                                                                               33.2%;
al Similarity 98.7%;
454; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
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TITLE
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UI-HF-BNO-akl-a-05-0-UI.rl NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077288 5', mRNA sequence.
AWS00047
ANSO0047.1 GI:7112287
EST.
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                                                                                                                                                                                                                                    315
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                                                                                                                                                                                                                                                                                                   591
                                                                                                                                                            Gaps
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                                                                                                                                                Score 421.4; DB 9; Length 434;
Pred. No. 1.3e-36;
0; Mismatches 1; Indels 1
 Amersham
primer: -28ml3 rev2 ET from
     High quality sequence stop: 386
          Location/Qualifiers
                                                                                                                                                 32.5%;
                                                                                                                                                      Similarity 99.5
33; Conservative
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62 ATAATGATCAATTGGTTTAACTTCTTTTATGTAAGTATGGTATATAAATTTCAAGACGAA

1263 aa 1264

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: ECO RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1455775, and 1500552-1502855). Subtraction by Bento Soares and M. Patima Bonaldo.
                                                                                                                                                                                                                    CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 480) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 TTGGCCTTGGGAAAAACCACGTTCTTCCTTTCCGATTCTTCATCCGGTCTAC-GCTATGC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
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Pred. No. 2.2e-40;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3643015"
/clone=lib="NCI_GGAP_Kidll"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 t
                                                                                                   fumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 474.
Location/Qualifiers
1.480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fatima Bonaldo.
53 c 9
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Best Local Similarity 99.4*
Matches 479; Conservative
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                                                             AUTHORS
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/lab_host="Cram."
//lab_host="Cram."
//lab_host="Cr
                                                                                                                        470 bp mRNA linear EST 29-JAN-1999 q170hl2.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1877735 3', mRNA sequence.
A1275149 A1275149:1 G1:3897423
                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummania; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 470)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. 470.
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1877735"
/clone=lib="soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 814 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ttcttatctctttcactttttaaatatctttcaccaggttatattttggtattattttc 1037
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Pred. No. 1.9e-39;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: -40UP from Gibco
High quality sequence stop: 437,
Location/Qualifiers
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98.3%;
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   2 CA 1
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us-09-762-249-13.rst

323 459 382 519 642 579 502	Oy 639 gractett Db 562 GCACTCTT RESULT 5 BF894780/C LOCUS LO	Nagaa. Nagaa. Goldman Brunst M.J. Simps Simps Souce JOURNAL Proc. MEDLINE 20202(COMMENT CONTA Ludwit Rua Pl	FEATURES Source	BASE COUNT ORIGIN
SOURCE Numan.	Φ	/Organism="Homo saplens" //db_xref="taxon:9506" //clone_lib="MT0132" //dev_stage="Adult" //dev_stage="Adul	99 gctggccgacgtgaaggcgcgcgcgcctcaacgagatcgagagccgcaccgcgallillillillillillillillillillillillilli	UV 279 cgaccaccoggocaggocaggggagggagggaggaggaggaggaggaggaggaggag

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/db_xref="taxon:9606"
/dbo=lib="MT0132"
/dev_stage="Adult"
/note="Crgan: marrow; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 from ORESTES PCR (U.S. Letters Patent application No. 196 into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bases I to 525)

NetC.E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
i,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
iman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
stein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
son,A.J.
gun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4780 525 bp mRNA linear EST 18-JAN-2001
MT0132-201100-497-509 MT0132 Homo sapiens CDNA, mRNA sequence.
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sequence was derived from the FAPESP/LICR Human Cancer Genome
ect. This entry can be seen in the following URL
p://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV1&t2=QV1-MT0132-
00-497-g09&t3=2000-11-20&t4=1)
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ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
nalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 525)
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ratory of cancer Genetics
ig Institute for Cancer Research
Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                 ottcagtaaagatagattcccacaaagttgtgcaatgtcattatatgacacctt 638
CGCCCATCCCAGACCATGGAGCGCGCTGGGAAGGACG-CACCAAAGCCGGGAG 381
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. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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quality sequence start: 23
quality sequence stop: 525.
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AUTHORS
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COMMENT
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sapiens cDNA clone IMAGE:5211074 3',
                 Note:
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                                                                                                                                                                                                                                                                                                            aagccgggagctctgccctgcagggagttgccccaacccttccggaactcagtctttag 508
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                                                                                          88
                                                                            1; Gaps
1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. this is a NIH,MC Library."
                                                                                         ccgagaacttgctggccgacgtgaagggcgcgcggccgcctcaacgagatcgagagcc
                                                                                                                                                                                                                   aaaagacggtcgactacaccggccaggccaaggcgcagtgcggaaggccgtgcagtacg
                                                                                                                                                                                                                                                                            420 AAGCCGGGAGCTCTGCCCTGCAGGGAGTTGCCCCAACCCTTTCCGGAACTCAGTCTTTAG
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                                                                                                                                                                                                                                                                                                                                                                                                             569 ataccgtccgatgattcttcagtaaagatagattcccacaaagttgtgcaatgtcattat
                                                            Length 739;
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                                                            Score 728; DB 10;
Pred. No. 1.4e-69;
0; Mismatches 0;
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603061815T1 NIH_MGC_118 F
mRNA sequence.
BI519530
BI519530.1 GI:15344322
EST.
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Best Local Similarity 99.9%;
Matches 739; Conservative
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/clone="Inmess:5211074"
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/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH MGC Library.
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      Euteleostomi;
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                                                                                         Collection (MGC)
                                                                                                                           Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
    Tissue Procurement: Life Technologies, Inc.
    CDNA Library Preparation: Life Technologies, Inc.
    CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.llnl.gov n column: 03
    Plate: LLAMISOS row: n column: 03
    High quality sequence start: 3
    High quality sequence stop: 890.
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  Chordata; Craniata; Vertebrata; Eutele
Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Verteb
Mammalia; Eutheria; Primates; Catarrhini; Homi
1 (bases 1 to 911)
NIH-MGC http://mgc.nci.nih.gov/.
Wational Institutes of Health, Mammalian Gene
Unpublished (1999)
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                                                                                                                                                                                                                                                                     AA262151 426 bp mRNA linear EST 13-AUG-1997 2S23d09.rl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:686033 5' similar to TR:G349315 G349315 SYNTAXIN 2''. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 426)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapps.remail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infoalmage.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Insert Length: 1332 Std Error: 0.00
Seq primer: -28m13 rev2 Er from Amersham
High quality sequence stop: 409.
Location/Qualifiers
                            255
                                                        398
                                                                                   315
                                                                                                                458
                                                                                                                                           374
             196 CGACTACACCGGCCAGGCCCAGGCGCAGGTGCGGAAGGCCGTGCAGTACGAGAGAAGAA
                                                       ccctgccggacctctgctgcttctgctgtctctgcctcaagtagcaggccggg
                                                                                                             256 CCCCTGCCGGACCCTCTGCTGCTTCTGCTGCCTGCCTCAAGTAGCAGGCCGGGC
                                                                                                                                                                    DB 9; Length 426;
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Pred. No. 1.5e-34;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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AA262151.1 GI:1898279
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Best Local S:
Matches 425,
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279
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Mismatches

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Conservative

425;

180

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AK017897 2219 bp mRNA linear HTC 19-JAN-2002 Mus musculus adult male thymus cDNA, RIKEN full-length enriched library, clone:5830405c08:homolog to SYNTAXIN 11, full insert
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                      307
                                                                                                                                                                                                                                  catggagcgcgctgggaaggacgtcaccaaagccgggagctctgccctgcagggagttgc 479
CATCCGCGACGTACACGAGCTCTTCTTGCAGATGGCGGTGCTGGTGGAGAAGCAGGCCGA 367
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                                           ggcgcaggtgcggaaggccgtgcagtacgaggagaagaaccctgccggaccctctgctg
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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AK017897
AK017897.1 GI:12857382
HTC; CAP trapper.
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AK017897
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AUTHORS
TITLE
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TITLE OF INVENTION: Methods and Compositions for Modulation
TITLE OF INVENTION: of Vesicular Release
NUMBER OF SEQUENCES: 35
CORRESSONDENCE ADDRESS:
ADDRESSED: Dehlinger & Associates
STREDT: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytoplasmic domain of Rat syntaxin 1A
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,985
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58.2%; Pred. No. 3e-17;
tive 0; Mismatches 148;
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Patent No. 5693476
GENERAL INFORMATION:
                                                                                                                                                                                                                   ATORNEY TRORMATION:
ATORNEY AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET UNBER: 8600-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 790 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Matches 206; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , NAME/KEY:
, LOCATION:
US-08-393-985-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-393-985-1
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat syntaxin 2 (GenBank L20823)
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Best Local Similarity 60.1%; Pred. No. 3.3e-18;
Matches 202; Conservative 0; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 gcgcaggtgcggaaggccgtgcagtacgaggagaag 336
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STREET: 350 Cambridge Avenue, Suite 250
                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0980
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 911 base pairs
APPLICATION NUMBER: US/08/393,985
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GENERAL INFOWATION:
APPLICANT: Scheller, Richard H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
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                                                            CLASSIFICATION: 435
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION:
US-08-393-985-5
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Length 790;

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Sequence 15, Application US/08690457

Patent No. 5726298

GENERAL INFORMATION:
APPLICANT: BIOMATERIAL RESEARCH INSTITUTE CO., LTD.
TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE SUBSTANCE
TITLE OF INVENTION: DESIGNATED AS EPIMORPHIN, GENES ENCODING THE SAME, AND ANTI
TITLE OF INVENTION: 14FRETO
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 124.8; DB 2;
Pred. No. 6.3e-19;
0; Mismatches 132;
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APPLICATION NUMBER: 135692/1992
FILING DATE: April 30, 1992
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
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APPLICATION NUMBER: 294856/1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08/078,309
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               April 17, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                              9.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.7
Matches 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                        SEQUENCE CHARACTERISTICS LENGTH: 870
                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Taya-cho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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US-08-628-187-12
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SOFTWARE: Patentl
                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                  TOPOLOGY:
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Patent No. 5837239

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF SEQUENCES:

TITLE SEGUENCES:

TITLE OF SEQUENCES:

TITLE OF SEQUENC
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ZIP: 244

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
'^*CMARE: PatentIn Release #1.0, Version #1.25
'^*CMARE: PatentIn Release #1.0, Version #1.25
'``TOM DATA: '``A'A'28,187
                                                                                                                                                                                                                                                                                                                                                                   Score 124.8; DB 1;
Pred. No. 6.3e-19;
0; Mismatches 132;
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APPLICATION NUMBER: 135692/1992
FILING DATE: April 30, 1992
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 870
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FILING DATE: October 16, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 294857/1991
FILING DATE: October 16, 1991
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APPLICATION NUMBER: 122906/1992
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Best Local Similarity 60.7
Matches 204; Conservative
                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
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us-09-762-249-13.rni

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Sequence 13, Application US/08690457

Patent No. 5726298
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BIONATERIAL RESEARCH INSTITUTE CO., LTD.
TITLE OF INVENTION: NOVEL PHYSTOLOGICALLY ACTIVE SUBSTANCE
TITLE OF INVENTION: THERETO
TITLE OF INVENTION: THERETO
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1, Taya cho, Sakae-ku, Yokohama-shi, KANAGAWA,
ADDRESSEE: Japan.
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    Gaps
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                                                                                                                                                                                                                                                                                                                                           625 ATCCGAGAGCTGCACGAGATGTTCATGGATATGGCCATGTTTGTCGAGACTCAGGGTGAA
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0; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CORRENT APPLICATION NUMBER: US/08/690,457 FILING DATE: 16-AUG-1996
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FILING DATE: April 17, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 135692/1992
FILING DATE: April 30, 1992
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/078,309
FILING DATE: June 15, 1993
APPLICATION NUMBER: 294856/1991
FILING DATE: October 16, 1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC: compatible
OPERATING SYSTEM: PC-DOS/MS-
    Matches 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
EDNESS: double
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Yokohama-shi
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TOPOLOGY: lin
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Patent No. 5837239

GENERAL INFORMATION:

APPLICANT: BIOMATERIAL RESEARCH INSTITUTE CO., LTD.

TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE SUBSTANCE DESIGNATED

TITLE OF INVENTION: AS EPIMORPHIN, GENES ENCODING THE SAME, AND ANTIBODIES THERETC

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: 1, Taya-cho, Sakae-ku, Yokohama-shi, KANAGAWA, Japan

STREE: 1, Taya-cho

CITY: Yokohama-shi
                                                                                                                                                                                                 565 AGGCAAGCTCTCAATGAGATCGAGTCCCGCCACAAGACATCATGAAGCTGGAGACCAGC 624
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                                                                                                                                                                                                                                                                                       505 CTGGAGAGCGGGAAGCCGTCCATCTTCATCTCGGATATTATATATCAGATTCACAAATCACT 564
                                                                                                                                                                        121 cgggccgcctcaacgagatcgagagccgccaccgcgaactgctgcgcctggagagccgc
      1 atccagcgccagctggagatcatgggcaaggaagtctcggggcgaccagatcgaggacatg
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Pred. No. 6.2e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      301 gcgcaggtgcggaaggccgtgcagtacgaggagaag 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      745 GAAGAGGAGGAAGAAAGCCATCAAATACCAGAGCAAG 780
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FILING DATE: April 5, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 294856/1991
FILING DATE: October 16, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 294657/1991
FILING DATE: October 16, 1991
PRIOR APPLICATION DATA:
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FILING DATE: April 17, 1991
PRIOR APPLICATION DATA:
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FILING DATE: APTIL 30, 1992
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Best Local Similarity
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121 cgggccgccctcaacgagatcgagagccgccaccgcgaactgctgcgcctggagagccgc 180
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                                                                                                                                                                                                                391 ATCCGAGAGCTGCACGAGATGTTCATGGATATGGCCATGTTTGTCGAGACTCAGGGTGAA 450
                                                                                                                                                                                                                                                              451 ATGGTCAACAACATCGAGAGAATGTGGTGAACTCCTGTAGATTACGTGGAACATGCCAAG 510
61 ttcgagcagggtaagtgggacgtgttttccgagaacttgctggccgacgtgaagggcgcg 120
                                                                                                            1 atccagcgccagctggagatcatgggcaaggaagtctcggggcgaccagatcgaggacatg
                                           271 CIGGAGAGCGGGAAGCCGTCCATCTTCATCTGGGATATTATATCAGATTCACAATCACT
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/493,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
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Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                  301 gcgcaggtgcggaaggccgtgcagtacgaggagaag 336
                                                                                                                                                                                                                                                                                                                                                                                           511 GAAGAGGAAGAAAGCCATCAAATACCAGAGCAAG 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 124.8;
Pred. No. 5.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hirai, Yohei
APPLICANT: Koshida, Shogo
APPLICANT: Oka, Yumiko
TITLE OF INVENTION: MODIFIED EPIMORPHIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08493071
Patent No. 6127149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22,685
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 711 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.6
Best Local Similarity 60.7
Matches 204; Conservative
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                                                                                                                                                 253 AGGCAAGCTCTCAATGAGATCGAGTCCCGCCACAAAGACATCATGAAGCTGGAGACCAGC
                                                             193 CTGGAGAGCGGGAAGCCGTCCATCTTCATCTCGGATATTATATCAGATTCACAAATCACT
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APPLICATION NUMBER: US/08/493,071
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60.7%; Pred. No. 5.3e-19;
iive 0; Mismatches 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hirai, Yohei
APPLICANT: Koshida, Shogo
APPLICANT: Oka, Yumiko
TITLE OF INVENTION: MODIFIED EPIMORPHIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
STREET: 99 CANAL CENTER PLAZA, SUITE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/08493071
Patent No. 6127149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 715-
TELECOMUNICATION INFORMATION:
TELECHONE: 703-684-1111
TELEFAX: 703-684-1124
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TYPE: nucleic acid
STRANDEDNESS: double
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STATE: VA
COUNTRY: USA
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Best Local Similarity
Matches 204; Conserv
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US-08-493-071-12
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Best Local Similarity 60.7%; Pred. No. 4.3e-13;
Matches 204; Conservative 0; Mismatches 132; Indels
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Search completed: September 24, 2002, 15:05:00 Job time: 3084 sec

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                                                                                                                                                                                                            Mus musculus
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                                                                                                           AAQ75248;
                                                                      RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            565 aggcaagctctcaatgagatcgagtcccgccacaaagacatcatgaagctggagaccagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  625 atccgagagctgcacgagatgttcatggatatggccatgtttgtcgaggactcagggtgaa
                                                                                                                                                                                                                                                                                                                                                                                                      This sequence encodes one of three isolated isoforms of mouse epimorphin, a protein produced by mesenchymal cells and which induces epithelial tissue morphogenesis. Modified forms of epimorphin in which the C-terminal hydrophobic region is replaced by a defective or non-hydrophobic peptide are also claimed. See also AAQ41592 and AAQ41594.
                                                                                        vascularisation; induction; epithelial tissue morphogenesis; ds.
                                                                                                                                                                                                                                                                                                                                                         its gene and antibodies - for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.6%; Score 124.8; DB 14;
60.7%; Pred. No. 4.3e-13;
11ve 0; Mismatches 132;
                                                                                                                                                          /product= epimorphin_isoform_A
                                                                                                                                                                                                                                                                                                                                                        Novel active substance epimorphin, its gene diagnosing and treating epithelial diseases
                                                                    Mouse epimorphin isoform A coding sequence
                                                                                                                                                                                                                                                                                       (BIOM-) BIOMATERIAL RES INST CO LTD.
                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 56; 76pp; Japanese.
                                                                                                                                                                                                                                                                                                          Takebe K;
            BP.
           AAQ41593 standard; cDNA; 867
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91JP-0294857.
92JP-0122906.
92JP-0135692.
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                                                 (first entry)
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                                                                                                           Mus musculus
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Best Local Simi
Matches 204;
                                                                                                                                                                                                                   15-OCT-1992;
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16-OCT-1991;
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                              AAQ41593;
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The sequence of the gene encoding mouse epimorphine isoform A. A DNA fragment (AAQ75250) containing the mouse epimorphine gene (AAQ75247) was isolated from a lambda-gtil expression cDNA library screened with a monoclonal antibody raised against mouse epimorphine. A probe (AAQ75243) derived from the mouse gene sequence was used to isolate isoforms of the mouse gene (AAQ75249.9) and the gene encoding human epimorphine (AAQ75244) and isoforms (AAQ75245.6). The genes were cloned into expression systems for the production of the protein in E.coli and in animal cells. The epimorphine can be used in the development of drugs to treat both congenital and acquired epidermal form abnormality.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe; epimorphine; human; mouse; lambda-gtll; expression library; monoclonal antibody; isoform; drug; congenital; acquired; E.coli; epidermal abnormality; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ttcgagcagggtaagtgggacgtgttttccgagaacttgctggccgacgtgaagggcgcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human or murine epimorphine - useful for development of c
treat congenital and acquired epidermal form abnormality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "sequence variance in isoform A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 867 BP; 261 A; 192 C; 245 G; 169 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16;
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                                                                     301 gcgcaggtgcggaaggccgtgcagtacgaggagaag 336
                                                                                                               Location/Qualiflers
793..867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse epimorphine isoform A gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 8; 41pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BIOM-) BIOMATERIAL KENKYUSHO KK
                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                     AAQ75248 standard; cDNA; 867
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Best Local Similarity 60.79
Matches 204; Conservative
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P-PSDB; AAR66480.
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                                to a second portion conty. At least a functional domain of epimorphin. The first portion may be selected from the peptides given in AAP82029 to AAR92045. The second portion may be full-length epimorphin. The first portion may be selected from the peptides given in AAP82029 to AAR92045. The second portion may be full-length epimorphin (see AAR92037 to AAR92045 for human and mouse epimorphins). Fragments (123), (2M), (3M) and (23) of epimorphin given in AAT16083 to AAT16090 are used in the prodn. of modified epimorphins.

123: N-terminus to right before C-terminal hydrophobic domain.

23: amino acid 30 to right before C-terminal hydrophobic domain.

23: amino acid 105 to right before C-terminal hydrophobic domain.

23: amino acid 105 to right before C-terminal hydrophobic domain.

23: amino acid 105 to right before C-terminal hydrophobic domain.

24: amino acid 105 to right before C-terminal hydrophobic domain.

25: amino acid 105 to right before C-terminal hydrophobic domain.

26: and treatment of morphogenetic abnormalities of epithelial tissue or novel remedies for wounds, eg burns, after surgery and for artificial corner.

27: Aley may also be used as components of cosmetics, hair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; mouse; epimorphin; coiled-coil region; functional domain; tissue, hydrophobic; deletion; truncation; regulation; morphogenesis; epithelium; artificial organ; cosmetic; hair tonic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ttcgagcagggtaagtgggacgtgttttccgagaacttgctggccgacgtgaagggcgcg 120
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                        contain a first portion of 5-99 amino acids joined
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                                                                                                                                                                                                                                                                                                                                                                                                             9.6%; Score 124.8; DB 17;
60.7%; Pred. No. 4.3e-13;
ive 0; Mismatches 132;
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                                                                                                                                                                                                                                                                                                                growth stimulators, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 564
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                                                                                                 Modified epimorphin and related DNA - useful e.g. for treatment of tissues or in artificial organs, or as an ingredient in cosmetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cgggccgccctcaacgagatcgagagccgccaccgcgaactgctgcgcctggagagccgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 798;
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 798 BP; 251 A; 177 C; 230 G; 140 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 124.8; DB 18;
Pred. No. 4.3e-13;
0; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                           as an ingredient in cosmetics, hair tonic, etc.
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/product= epimorphin_isoform_B
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                                                                                                                                                   Example 1; Page 14; 18pp; Japanese.
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                                 SUME ) SUMITOMO ELECTRIC IND
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95JP-0099980
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Matches 204; Conservative
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31-MAR-1995;
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gcgcaggtgcggaaggccgtgcagtacgaggagaag 336 gaagagacgaagaaagccatcaaataccagagcaag

BP.

** SEX BX BX S

(first entry)

181 atccgcgacgtacacgagctcttcttgcagatggcggtgctggtggagaagcaggccgac 240

391 atccgagagctgcacgagatgttcatggatatggccatgtttgtcgagactcagggtgaa 241 accetgaacgtcatcgagetcaacgtacaaagacggtcgactacaccggccaag

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Epimorphin; human; mouse; wound; burn; epithelial tissue; diagnosis; treatment; morphogenetic abnormality; cosmetic; hair growth stimulator; ds.
                                                                                                                                                                                                                                                                                                                                                                      Mouse epimorphin fragment (2M)
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                                                                                                                                                                                                                                                                  AAT16086 standard; cDNA; 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hirai Y, Koshida S,
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P-PSDB; AAR92046.
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                                                                                                                                                                                                                                                                                                                                     30-MAY-1996
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31-MAR-1995;
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                                                                                                                                                                                                                                                                                Human; mouse; epimorphin; coiled-coil region; functional domain; tissue;
hydrophobic; deletion; truncation; regulation; morphogenesis; epithelium;
artificial organ; cosmetic; hair tonic; ds.
451 atggtcaacaacatcgagagaaatgtggtgaactctgtagattacgtggaacatgccaag 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified epimorphin and related DNA – useful e.g. for treatment of
tissues or in artificial organs, or as an ingredient in cosmetics
                                                                                                                                                                                                                                                    Mouse epimorphin truncated variant, 3M coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 564 BP; 181 A; 124 C; 162 G; 97 T; 0 other;
                               301 gcgcaggtgcggaaggccgtgcagtacgaggagaag 336
                                                                511 gaagagacgaagaaagccatcaaataccagagcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 13; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SUME ) SUMITOMO ELECTRIC IND
                                                                                                                                                  AAT62412 standard; cDNA; 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95JP-0175540.
95JP-0099980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            96JP-0099684
                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-220419/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAW14261
                                                                                                                                                                                                                                                                                                                                                                                        JP09065885-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUN-1995;
31-MAR-1995;
                                                                                                                                                                                                                   02-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tonic, etc.
                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                  AAT62412;
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New polypeptides contain a first portion of 5.99 amino acids joined to a second portion contg. at least a functional domain of epimorphin. The first portion may be selected from the peptides given in AR892029 to AA892036. The second portion may be full-length epimorphin (see AA892037 to AA892042 for human and mouse epimorphins). Fragments (123), (2M), (3M) and (23) of epimorphin given in AA716083 to AA716090 are used in the prodn. of modified epimorphins.

123: N-terminus to right before C-terminal hydrophobic domain.

23: amino acid 79 to right before C-terminal hydrophobic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and treatment of morphogenetic abnormalities of epithelial tissue or novel remedies for wounds, eg burns, after surgery and for artificial organs. They may also be used as components of cosmetics, hair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The modified epimorphins are useful for the development of diagnosis
Novel polypeptide containing an epimorphin functional domain - has possible benefits in epithelial tissue treatments, e.g. burns and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 711 BP; 232 A; 155 C; 201 G; 123 T; 0 other;
                                                                                                                                                                                                           Claim 27; Page 30; 62pp; English.
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                                                                                                            for artificial organs
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Indels

132;

0; Mismatches

Best Local Similarity 60.7 Matches 204; Conservative

Similarity

Query Match

9.6%; Score 124.8; DB 18; Length 564; 60.7%; Pred. No. 4e-13;

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1 atccagcgccagctggagatcatgggcaaggaagtctcggggcgaccagatcgaggacatg 60

cgggccgccctcaacgagatcgagagccgccaccgcgaactgctgcgcctggagagccgc 180

121

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271 ctggagaggggaagccgtccatcttcatctcggatattatatcagattcacaaatcact

8

Oka Y;

95JP-0099980. 94JP-0162874. 95JP-0099979.

95EP-0304270.

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                                      AA261474-87 represent tumour suppressor activated pathway gene CDNAs, designated TSAP9-TSAP22, respectively. The cellular expression of TSAP genes is induced during apoptosis and tumour suppression. The specification also describes a tumour suppressor inhibited pathway gene TSIP3. Medicaments comprising either vectors for cellular expression of that ensure cellular expression of these genes, or compounds that inhibit cellular expression of these genes, or compounds that inhibit cellular expression of these genes are useful for treating cancer or as antiviral agents. Probes and primers derived from the genes and antigens or antibodies corresponding to TSAP or TSIP proteins are useful for diagnostic purposes, especially for identifying a predisposition to cancer and for monitoring cancer. Cells transformed with TSAP or TSIP genes can be used to screen for anticancer and
                                                                                                                                                                                                                                                                                                             685 atctgactgtagggtgaatgtctgaggcctgcctcctaataaagactcaaggaggaagtc 744
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                   2 atctgactgtagggtgaatgtctgaggcctgcctcctaataaagactcaaggaggaagtc 61
                                                                                                                                                                                                                                                                                                                                                                                               922
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                                                                                                                                                                                                                              DB 21; Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 240 BP; 68 A; 54 C; 47 G; 71 T; 0 other;
                                                                                                                                                                                                                             16.2%; Score 209.2; DB 2:
97.9%; Pred. No. 5.7e-28;
Live 0; Mismatches 3
during apoptosis and/or tumour suppression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Epimorphin; human; mouse; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT16088 standard; cDNA; 486 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epimorphin fragment (23).
                   Claim 1; Page 21; 24pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SUME ) SUMITOMO ELECTRIC IND
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94JP-0162874.
95JP-0099979.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95EP-0304270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                    Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koshida S,
                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                            antiviral agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-1995;
21-JUN-1994;
31-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis;
hair growt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hirai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT16088;
                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                  181
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AAT16088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; mouse; epimorphin; colled-coil region; functional domain; tissue; hydrophobic; deletion; truncation; regulation; morphogenesis; epithelium; artificial organ; cosmetic; hair tonic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ttcgagcagggtaagtgggacgtgttttccgagaacttgctggccgacgtgaagggcgcg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atggtcaacaacatcgagagaaatgtggtggtgactctgtagattacgtggaacatgccaag 432
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                                                                                      Novel polypeptide containing an epimorphin functional domain - has possible benefits in epithelial tissue treatments, e.g. burns and for artificial organs
                                                                                                                                                                                                                                                            New polypeptides contain a first portion of 5-99 amino acids joined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atccgagagctgcacgagatgttcatggatatggccatgtttgtcgagactcagggtgaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atccgcgacgtacacgagctcttcttgcagatggcggtgctggtggagaagcaggccgac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 486 BP; 152 A; 110 C; 139 G; 85 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 124.8; DB 1
Pred. No. 3.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 gcgcaggtgcggaaggccgtgcagtacgaggagaag 336
                                                                                                                                                                                                     Claim 27; Page 32; 62pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               growth stimulators, etc.
WPI; 1996-118213/13.
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                              P-PSDB; AAR92048
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/note='fragment (3M) is derived 79-265 aa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       egggeegecetcaacgagategagageegecacegegaactgetgegeetggagageege 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product='Epimorphin fragment designated
(3M)'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331 AGGCAAGCTCTCAATGAGATCGAGTCCCGCCACAAAGACATCATGAAGCTGGAGACCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 CTGGAGAGCGGGAAGCCGTCCATCTTCATCTCGGATATTATATCAGATTCACAAATCACT
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PN JP 199/002000
PD 11-MAR-1997
PF 29-MAR-1996 JP 1996099684
PR 31-MAR-1995 JP 95P 99880, 19-JUN-1995 JP 95P
PR 31-MAR-1995 JP 95P 99880, 19-JUN-1995 JP 95P
KOSHIDA SHOGO, OKA YUMIKO, HIRAI YOHEI
PC C12N15/09,C07H21/04,C07K7/06,C07K7/08,C07K14/485,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 564;
                                                                                                                                                                                                                   'organism='Artificial sequences'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.6%; Score 124.8; DB 6; 60.7%; Pred. No. 4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 132;
                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gegeaggtgeggaaggeegtgeagtaegaagaag 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           511 GAAGAGGAGGAAGAAGCCATCAAATACCAGAGCAAG 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 711)
Hirai,Y., Koshida,S. and Oka,Y.
Modified epimorphin
Patent: US 6127149-A 11 03-OCT-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AR111442 711 bp
Sequence 11 from patent US 6127149.
AR111442
                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                              /organism="unidentified"
/db_xref="taxon:32644"
124 c 162 q 97
                                                                                                                                                                                                                                                                                                                   Epimorphin'.
                                                                               PC C12N15/09, C07H21/04, C07H21/02, C07H21/02, C12P21/02, C12P1:19); CC strandedness: Double; CC topology: Linear; FH Key Location FH Source 1. .564 FT
                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                          monse
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                                                                                                                                                                                                                                     mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                    PAT 14-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 atccgcgacgtacacgagctcttcttgcagatggcggtgctggtggagaagcaggccgac 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ttcgagcagggtaagtgggacgtgttttccgagaacttgctggccgacgtgaagggcgcg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 ATCCAGCGCCAGCTGGAGATCACTGGGAGGACCACCACTGACGACGAGGAGGAGGATG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 CTGGAGAGCGGGAAGCCGTCCATCTTCATCTCGGATATTATATCAGATTCACAAATCACT 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 atccagcgccagctggagatcatgggcaaggaagtctcggggcgaccagatcgaggacatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 124.8; DB 6; Length
Pred. No. 4e-10;
0; Mismatches 132; Indels
                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               564 bp DNA lir
DNA encoding mouse Epimorphin-derived peptide.
E12727
E12727.1 GI:3251559
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RES KOSHÍGA,S., OKA,Y. and Hiral,Y...

TALLORED DERIVATIVE OF EPIMORPHIN

L PATENT: JP 1997065885-A 6 11-MAR-1997;

SUMITOMO ELECTRIC IND LTD

OS ATTICL
               301 gcgcaggtgcggaaggccgtgcagtacgaggagaag 336
                                    DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 gcgcaggtgcggaaggccgtgcagtacgaggagaag 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           511 GAAGAGGAAGAAAGCCATCAAATACCAGAGCAAG 546
                                                                                                                                                                                                                                                               1 (bases 1 to 564)
Hiral,Y., Koshida,S. and Oka,Y.
Modified epimorphin
Patent: US 6127149-A 12 03-OCT-2000;
Location/Qualifiers
                                                                                                                                AR111443 564 bp 18
Sequence 12 from patent US 6127149.
AR111443
                                                                                                                                                                                                                                                                                                                                                                                     97
                                                                                                                                                                                                                                                                                                                                                              /organism="unknown"
124 c 162 q
                                                                                                                                                                               AR111443.1 GI:12828291
                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 204; Conservative
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unidentified.
unidentified
                                                                                                                                                                                                                                                   Unclassified.
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VERSION
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AR111443
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BASE COUNT

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AUTHORS

JRNAL

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ACCESSION VERSION KEYWORDS

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RESULT 13

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REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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polyA_site

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1. .825
/note="syntaxin 2', differs from syntaxin 2 and 2' only at
the carboxyl terminal end in the transmembrane region"
/codon_start=""".","
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /traislation="MedripdLtacrkSddgdnavIITvekdhfwdaffhqveeIrsS
IartaghybdykknisIIISaPnpecKIKEELbLukEIKKTANRIRCKLKALEOSCD
QdbucnrtsydlrirrqusylsrktyvbywteyneaQilfrerskGriokOLEITGRT
TydbeilebwlesGryofifiSDIITSDSQITRQALNEIESSHKOIMKLFTSIREHHBWFN
DMAMFVETQGEWYNNIERNVVNSVDYVEHAKEETKKAIKYQSKARRGVLCALGROC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROD 26-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                1017 tatattttggtattattttccaaacatttttaagcactgaatatcgaacaagcactcaa 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 825)
Bennett, M.K., Garcia-Arraras, J.E., Elferink, L.A., Peterson, K., Fleming, A.M., Hazuka, C.D. and Scheller, R.H.
The syntaxin family of vesicular transport receptors C211 74 (5), 863-873 (1993)
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                      1 atccagcgccagctggagatcatgggcaaggaagtctcggggcgaccagatcgaggacatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L20888.1 GI:349314
syntaxin 2; vesicular transport receptor.
Rattus norvegicus (library: lambda Zap II) cDNA to mRNA.
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Pred. No. 6.9e-12;
); Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     825;
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Pred. No. 3.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RATSYNTX2B 825 bp mF
Rattus norvegicus syntaxin 2'' mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10116"
/tissue_lib="lambda Zap II"
1. 825
                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                 48
                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human"
1. 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAA03048.1"
/db_xref="G1:349315"
                                                                                                                                                                                                                                                                                                                                                                                                  tttttacttgattacatatgcacatgtatg 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                    30 TTTTTACTTGATTACATATGCACATGTATG 1
                                                                                                              complement(134. .156)
22 c 21 g
Location/Qualifiers
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94.0%;
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primer_bind
COUNT
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ORIGIN
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AUTHORS
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MEDLINE
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KEYWORDS
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                                                                                                                 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                             cctgaaaattccctggttctgttccattttgagcgaaattggccttgggaaaaaccacgt 864
                                                                                                                                                                                                                                                                                                                  121 CCTGAAAATTCCCTGGTTCTGTTCCATTTTGAGCGAAATTGGCCTTGGGAAAAACCACGT 180
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                865 tetteettteegattetteateeggtetaeggetatgeaatteeteeeaaatataga 922
                                                                                                                                                                                                                                                                                                                                                                   Prepared with primer pairs derived from THC120341: GenBank
Accession Numbers- R65594, R33852, T25062, L70341.
                                                                                                                 7
                                                                                Length 240;
                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MD 20850
                                                                    Score 209.2; DB 9;
Pred. No. 2.5e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenomicDNA: 25 ng
Primer: 0.43 uM each
dNTPS: 230 uM each
AmpliTaq: 0.5 units
TagStart Ab: 0.5 units
Total Volume: 10 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96C 5min
54C 30sec
72C 30sec
95C 30sec
72C 5min
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Enail: mdadams@tigr.org
Primer A: CATACATGTGCATATGTAATCAA
Primer B: CGGGTATATTTGGGTATTATT
STS size: 156
PCR Profile:
                                                                                                                0; Mismatches
               71
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               Б
               47
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FinalExtend:
                                                                              Query Match
Best Local Similarity 97.9%;
Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G32623.1 GI:5923144
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Human STS sequences
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Mark Adams
               Ö
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              68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human.
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VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT REFERENCE AUTHORS

DEFINITION

ACCESSION

RESULT G32623/c

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538 accagectgtgettggaaagatggttagttgatacegteegatgattetteagtaaagat 597
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                                                                                                                                                                                                                                                                                                                                                                                         ttcgagcagggtaagtgggacgtgttttccgagaacttgctggccgacgtgaagggcgcg
                                                                                                                                                                                                                                                                                             Length 207379;
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s: contig of 10807 bp in length as contig of 9788 bp in length grap of unknown length contig of 12076 bp in length contig of 12076 bp in length contig of 11761 bp in length gap of unknown length contig of 12986 bp in length contig of 12986 bp in length contig of 14045 bp in length gap of unknown length contig of 14045 bp in length gap of unknown length gap of unknown length contig of 14045 bp in length gap of unknown length
                                                                                                                                                                                                                                    /clone_lib="RPCI mouse BAC library 23"
45400 c 44678 g 56655 t 2873 others
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                             Score 397.2; DB 2;
Pred. No. 3.6e-52;
0; Mismatches 383;
                                                                                                                                                                             musculus"
                                                                                                                                                                                                  /db_xref="taxon:10090"
/chromosome="10"
/clone="rp23-111d4"
                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                            /organism="Mus mus/strain="C57BL/6J
                                                                                                                                                                                                                                                                                              30.7%;
65.5%;
                                              152889:
152989:
164750:
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191981:
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                                                                                                                            Direct Submission
Submitted (17-WAY-2001) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
On Jan 29, 2002 this sequence version replaced gi:17861042.
                                    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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The University Of Oklahoma
Center code: UOKNOR
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5683: contig o
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Direct Submission
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42501. 42588
/note="44 copies 2 mer tt 73% conserved"
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/note="FRAM repeat: matches -1. .176 of consensus"
43597. 44315
/note="Alusx repeat: matches 1. .309 of consensus"
45682. 43536
/note="Alusq repeat: matches 1. .313 of consensus"
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/note="Ray repeat: matches 1. .310 of consensus"
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Yoo,J.-S. and Scheller,R.H.

Direct Submission
Submitted (22-JAN-1998) Molecular and Cellular Physiology, Stanford
University, Stanford, CA 94305, USA
Location/Qualifiers
1. 1280
/organism="Homo sapiens"
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Advani,R.J., Bae,H.R., Book,J.B., Chao,D.S., Doung,Y.C., Prekeris,R., Yoo,J.S. and Scheller,R.H.
Seven novel mammalian SNARE proteins localize to distinct membrane
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/cell_type="germinal B cell"
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/protein_id="AAC24031.1"
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Amson, R.B.
Direct Submission
Submitted (22-CCT-1998) Amson R.B., Tumor Suppression, CEPH Human
Submitted (22-CCT-1998) Amson R.B., Tumor Suppression, CEPH Human
Polymorphism Study Center, 27 rue Juliet Dodu Paris, 75010, FRANCE
Location, Qualifiers
                                                                                                                                                                                                               ttcgagcagggtaagtgggacgtgtttccgagaacttgctggccgacgtgaaggg-cgc 119
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Pred. No. 1.2e-190;
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                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="K562"
                                                                     /clone="TSAP21 extended"
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corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is a mannotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Emm., EMBL: Sw., SWISSPROT: Tr., TREMBL: Wp:, WORMPEP: Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear PRI 02-FEB-2001
on chromosome 6, complete
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On Feb 5, 2001 this sequence version replaced gi:12214260.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
bykaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 104228)
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                                                                                                 aaattggccttgggaaaaaccacgttcttcctttccgattcttcatccggtctacggcta
117 104228 bp DNA DNA sequence from clone RP1-83M4
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AL135917.15
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Human DNA
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Search completed: September 24, 2002, 14:59:34 Job time: 7593 sec